

Replacement Sheet 09/820,788

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1 CCTGCCTGGT CCTCTGTGCC TGGTGGGGTG GGGGTGCCAG GTGTGTCCAG
51 AGGAGCCCAT TTGGTAGTGA GGCAGGTATG GGGCTAGAAG CACTGGTGCC
101 CCTGGCCGTG ATAGTGGCCA TCTTCCTGCT CCTGGTGGAC CTGATGCACC
151 GGCGCCAACG CTGGGCTGCA CGCTACTCAC CAGGCCCCCT GCCACTGCCC
201 GGGCTGGGCA ACCTGCTGCA TGTGGACTTC CAGAACACAC CATACTGCTT
251 CGACCAAGTT CGGCGCCGCT TCGGGGACGT GTTCAGCCTG CAGCTGGCCT
301 GGACGCCGGT GGTCTGTGCT AATGGGCTGG CGGCCGTGCG CGAGGCGCTG
351 GTGACCCACG GCGAGGACAC CGCCGACCGC CCGCCTGTGC CCATCACCCA
401 GATCCTGGGT TTTGGGCCGC GTTCCCAAGG ACGCCCTTT CGCCCCAAGC
451 GTCTCTTGA CAAAGCCGTG AGCAACGTGA TCGCCTCCT CACCTGCGGG
501 CGCCGCTTCG AGTACGACGA CCCTCGCTTC CTCAGGCTGC TGGACCTAGC
551 TCAGGAGGGA CTGAAGGAGG AGTCGGGCTT TCTGCGCGAG GTGCTGAATG
601 CTGTCCCGT CCTCTGTCAT ATCCCAGCGC TGGCTGGCAA GGTCTTACGC
651 TTCCAAAAGG CTTTCCTGAC CCAGCTGGAT GAGCTGCTAA CTGAGCACAG
701 GATGACCTGG GACCCAGCCC AGCCCCCCCG AGACCTGACT GAGGCCTTCC
751 TGGCAGAGGC AGAGAAGGCC AAGGGGAACC CTGAGAGCAG CTTCAATGAT
801 GAGAACCTGC GCATAGTGGT GGCTGACCTG TTCTCTGCCG GGATGGTGAC
851 CACCTCGACC ACGTGGCCT GGGCCTCCT GCTCATGATC CTACATCCGG
901 ATGTGCAGCG CCGTGTCCAA CAGGAGATCG ACGACGTGAT AGGGCAGGTG
951 CGGCGACCGA AGATGGGTGA CCAGGCTCAC ATGCCCTACA CCACTGCCGT
1001 GATTCATGAG GTGCAGCGCT TTGGGGACAT CGTCCCCCTG GGTGTGACCC
1051 ATATGACATC CCGTGACATC GAAGTACAGG GCTTCCGCAT CCCTAAGGGA
1101 ACACACTCA TCACCAACCT GTCATCGGTG CTGAAGGATG AGGCCGTCTG
1151 GCGAAGCCC TTCCGCTTCC ACCCGAACA CTCTCTGGAT GCCCAGGGCC
1201 ACTTTGTGAA GCCGGAGGCC TTCTGCTT TCTCAGCAGG CCGCCGTGCA
1251 TGCCTCGGG AGCCCTGGC CGCATGGAG CTCTTCTCT TCTTCACTC
1301 CCTGCTGCAG CACTTCAGCT TCTCGGTGCC CACTGGACAG CCCCAGGCCA
1351 GCGACCATGG TGTCTTTGCT TTCTTGGTGA CCCCATCCC CTATGAGCTT
1401 TGTGCTGTGC CCCGCTAGAA TGGGGTACCT AGTCCCCAGC CTGCTCCCTA
1451 GCCAGAGGCT CTAATGTACA ATAAAGCAAT GTGGTAGTTC CAAAAAATAA
1501 AAAAAAATAA AAAAAAATAA AAAAAAATAA AAAAAAATAA
(SEQ ID NO: 1)

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FEATURES:

5'UTR: 1 - 77
 Start Codon: 78
 Stop Codon: 1416
 3'UTR: 1419

Homologous proteins:

Top 10 BLAST Hits

	Score	E
CRA 18000004889269 /altid=gi 181304 /def=gb AAA53500.1 (M33388...	884	0.0
CRA 18000004927597 /altid=gi 4503223 /def=ref NP_000097.1 cyto...	883	0.0
CRA 18000004923926 /altid=gi 181306 /def=gb AAA35737.1 (M33189...	864	0.0
CRA 18000005007118 /altid=gi 2493367 /def=sp Q29488 CPDH_MACFA ...	827	0.0
CRA 18000005100319 /altid=gi 3913340 /def=sp O18992 CPDJ_CALJA ...	800	0.0
CRA 18000004884804 /altid=gi 486997 /def=pir S37284 cytochrome...	682	0.0
CRA 18000004889271 /altid=gi 522195 /def=gb AAA36403.1 (M24499...	673	0.0
CRA 18000004884803 /altid=gi 461826 /def=sp Q01361 CPDE_BOVIN C...	669	0.0
CRA 18000004939934 /altid=gi 117244 /def=sp P13108 CPD4_RAT CYT...	665	0.0
CRA 18000005107537 /altid=gi 2575863 /def=dbj BAA23125.1 (AB00...	665	0.0

EST:

	Score (bits)	E Value
Sequences producing significant alignments:		
gi 9872134 /dataset=dbest /taxon=960...	775	0.0
gi 6144331 /dataset=dbest /taxon=9606 ...	648	0.0
gi 6703894 /dataset=dbest /taxon=9606 ...	648	0.0

EXPRESSION INFORMATION FOR MODULATORY USE:

gi|9872134 /liver
 gi|6144331 /kidney
 gi|6703894 /lung

Tissue Expression:

Whole Liver

FIGURE 1

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1 MGLEALVPLA VIVAIFLLLV DLMHRRQRWA ARYSPGPLPL PGLGNLLHVD
51 FQNTPYCFDQ LRRRFGDVFS LQLAWTPVVV LNGLAAVREA LVTHGEDTAD
101 RPPVPITQIL GFGPRSQGRP FRPNGLLDKA VSNVIASLTC GRRFEYDDPR
151 FLRLDLAQE GLKEESGFLR EVLNAVPLVLL HIPALAGKVL RFQKAFLTQL
201 DELLTEHRMT WDPAQPPRDL TEAFLAEMEK AKGNPESSFN DENLRIVVAD
251 LFSAGMVTTS TTLAWGLLLM ILHPDVQRRV QQEIDDVIGQ VRRPEMGDQA
301 HMPYTTAVIH EVQRFGDIVP LGVTHMTSRD IEVQGFRIPI GTTLITNLSS
351 VLKDEAVWEK PFRFHPEHFL DAQGHFVKPE AFLPFSAGRR ACLGEPLARM
401 ELFLFFTSLL QHFSFSVPTG QPRPSHHGVF AFLVTPSPYE LCAVPR
(SEQ ID NO: 2)

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FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

347-350 NLSS

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

327-329 TSR

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 5

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1      93-96 THGE
2     198-201 TQLD
3     238-241 SFND
4     327-330 TSRD
5     437-440 SPYE

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[4] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 2

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1     233-238 GNPES
2     255-260 GMVTS

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[5] PDOC00009 PS00009 AMIDATION
Amidation site

Number of matches: 2

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1     140-143 CGRR
2     387-390 AGRR

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[6] PDOC00081 PS00086 CYTOCHROME_P450
Cytochrome P450 cysteine heme-iron ligand signature

385-394 FSAGRRACLG

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	3	23	1.877	Certain
2	68	88	1.096	Certain
3	171	191	0.668	Putative
4	252	272	1.914	Certain
5	400	420	1.402	Certain
6	425	445	0.833	Putative

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BLAST Alignment to Top Hit:

>CRA|18000004889269 /altid=gi|181304 /def=gb|AAA53500.1| (M33388)
 cytochrome P450 IID6 [Homo sapiens] /org=Homo sapiens
 /taxon=9606 /dataset=nraa /length=497
 Length = 497

Score = 884 bits (2259), Expect = 0.0
 Identities = 444/497 (89%), Positives = 445/497 (89%), Gaps = 51/497 (10%)

Query: 1 MGLEALVPLAVIVAIFLLLVDMHRRQRWAARYSPGGLPLPGLGNLLHVDQNTPYCFDQ 60
 MGLEALVPLAVIVAIFLLLVDMHRRQRWAARY PGGLPLPGLGNLLHVDQNTPYCFDQ
 Sbjct: 1 MGLEALVPLAVIVAIFLLLVDMHRRQRWAARYPPGGLPLPGLGNLLHVDQNTPYCFDQ 60

Query: 61 LRRRFGDVFSQLAWTPVVVLNGLAAVREALVTHGEDTADRPPVPITQILGFGPRSQG-- 118
 LRRRFGDVFSQLAWTPVVVLNGLAAVREALVTHGEDTADRPPVPITQILGFGPRSQG
 Sbjct: 61 LRRRFGDVFSQLAWTPVVVLNGLAAVREALVTHGEDTADRPPVPITQILGFGPRSQGVF 120

Query: 119 -----RPFRRPNGLLDK 129
 RPFRRPNGLLDK
 Sbjct: 121 LARYGPWREQRFSVSTLRNLGLGKKSLEQWVTEEAACLCFAFANHSGRPFRRPNGLLDK 180

Query: 130 AVSNVIASLTCGRREFYDDPRFLRLDLAQEGLKEESGFLREVLNAVVPVLLHIPALAGKV 189
 AVSNVIASLTCGRREFYDDPRFLRLDLAQEGLKEESGFLREVLNAVVPVLLHIPALAGKV
 Sbjct: 181 AVSNVIASLTCGRREFYDDPRFLRLDLAQEGLKEESGFLREVLNAVVPVLLHIPALAGKV 240

Query: 190 LRFQKAFSLTQDELLEHRTWDPAPPRDLTEAFLAEMEAKAGNPESFNDENLRIVVA 249
 LRFQKAFSLTQDELLEHRTWDPAPPRDLTEAFLAEMEAKAGNPESFNDENLRIVVA
 Sbjct: 241 LRFQKAFSLTQDELLEHRTWDPAPPRDLTEAFLAEMEAKAGNPESFNDENLRIVVA 300

Query: 250 DLFSAGMVTSTTTLAWGLLLMILHPDVQRRVQOEIDDVIGQVRRPEMGDQAHMPYTTAVI 309
 DLFSAGMVTSTTTLAWGLLLMILHPDVQRRVQOEIDDVIGQVRRPEMGDQAHMPYTTAVI
 Sbjct: 301 DLFSAGMVTSTTTLAWGLLLMILHPDVQRRVQOEIDDVIGQVRRPEMGDQAHMPYTTAVI 360

Query: 310 HEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKGTTLITNLSSVLKDEAVWEKPFRRHPEHF 369
 HEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKGTTLITNLSSVLKDEAVWEKPFRRHPEHF
 Sbjct: 361 HEVQRFGDIVPLGVTHMTSRDIEVQGFRIPKGTTLITNLSSVLKDEAVWEKPFRRHPEHF 420

Query: 370 LDAQGHFVKPEAFLPFSAGRRACLGEPLARMELFLFFTSLLQHFSFSVPTGQPRPSHHGV 429
 LDAQGHFVKPEAFLPFSAGRRACLGEPLARMELFLFFTSLLQHFSFSVPTGQPRPSHHGV
 Sbjct: 421 LDAQGHFVKPEAFLPFSAGRRACLGEPLARMELFLFFTSLLQHFSFSVPTGQPRPSHHGV 480

Query: 430 FAFLVTPSPYELCAVPR 446
 FAFLV+PSPYELCAVPR
 Sbjct: 481 FAFLVSPSPYELCAVPR 497 (SEQ ID NO: 4)

Hmmer search results (Pfam):

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
PF00067	Cytochrome P450	516.7	1.7e-151	2

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF00067	1/2	35	113	..	1 92 [.	78.1	2.7e-21
PF00067	2/2	117	443	..	150 497 .]	442.7	3.3e-129

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1 AGCCTTACAA AGTGCTGGGA TTACCTGCGT GAGCCACCGG GTCCGGCCTC
51 TTTATGTCTT ACTGTA CTGTCTTGAA AAGTACTTAT TATTTTGTAT
101 TGGTTCATCA TTTAGTCTAA TTAAATAAAG AGTAGTTTAC ACACCACAAT
151 TACAGTATTA TAATACTCTG TTTTCTGTG TGCTTACTAT TACCAGTGAG
201 TTTGTACCT TTAGATGATT TCTTCTTGCT CATTAAATATC CTTTTTTTTT
251 TCAGATTGAA AAACCTCCCT TAGCATTTCT TGTGGGATAT AGGTCTGGTG
301 TTGATGAAAT CTCGAGCTT TTGTTTGTCT GGAAGGTCT TATTTCTCC
351 TTCCTGTTGG AAGGATATTT TTGCCAGATA CGTTATTCTA GGCTAAAAGT
401 TTTTTTCTC TCAGCACTTT AAATATGTCA TGCCACTCCC CCCTGGCCTG
451 TAAGGTTTCC ACTGAAAGG TGGCTGCCCC ATGTCATGTA TTGGAGCTCT
501 ACTGCATGTT ATTTGTTTCT TTTCTTTGCG TGCTTTTAGG ATCCTTTCTT
551 TATCCTTGAG CTTTCGGAGT TTAATTATCA GATGCCTTGA GGTCTCTTTC
601 TTTGGGTTAA ATCTGCTTGG TGTCTATAA ACTTCTTGTA CAAAAATCA
651 GCCAGGCATG GTGGTGGGCA CCTGTAATCC CAGCTACTTG GGAGGCTGAG
701 GCAGGAGAAT CGCTGAACC CTGGAGGTGG AGGTGTCAGT GAGCCGAGAT
751 CGCATCATTT CACTCCCACC TGGCGGACAG AGCAAAACTC CGTCTCAAAA
801 AAAAAATTAT TTGGGCTCGG TGGTGCTGT AGTCCCAGCT ACTTGGGAGG
851 CAGGAGGTCC ACTTGATGTT GAGATTGCAG TGAGCCATGA TCCTGCCACT
901 GCACTCCGGC CCGGGCAACA GAGTGAGACC CTGTCTAAAG AAAAAATAAA
951 AATAAAAAAG CAACATATCC TAAATAAAGG ATCCTCCATA ATGTTTCCAC
1001 CAGATTTCTA ATCAGAAACA TGGAGGCCAG GAAGCAGTGG AGAATGACGA
1051 CCCTCAGGCA GCCCTGGAGG ATGCTGTAC AGGCTGGGGC AAGGGCCTTC
1101 AGGCTACCAA CTGGGAGCTC TGGGAACAGC CCTGTTGCAA ACAGGAAGTC
1151 ATGGCCCGG CAGAGCCCAG AATGTGGGCT GAGCTGGGAT CCATGTGACA
1201 GCTTTGAGGC TCACCGGGAG CAGCCTCTGG ACAGGAGAGG TCCCATCCAG
1251 GAAACCTCGG GCATGGCTGG GAAGTGGGGT ACTTGGTGCC GGGTCTGTAT
1301 GTGTGTGTGA CTGGTGTGTG TGAGAGAGAA TGTGTGCCCT GAGTGTCACT
1351 GTGAGTCTGT GTATGTGTGA ATATTGTCTT TGTGTGGGTG ATTTTCTGCA
1401 TGTGTAATCG TGTCCCTGCA AGTGTGAACA AGTGGACAAG TGTCTGGGAG
1451 TGGACAAGAG ATCTGTGCAC CATCAGGTGT GTGCATAGCG TCTGTGCATG
1501 TCAAGAGTGC AAGGTGAAGT GAAGGGACCA GGCCCATGAT GCCACTCATC
1551 ATCAGGAGCT CTAAGGCCCC AGGTAAGTGC CAGTGACAGA TAAGGGTGCT
1601 GAAGGTCACT CTGGAGTGGG CAGGTGGGGG TAGGGAAAGG GCAAGGTCAT
1651 GTTCTGGAGG AGGGGTTGTG ACTACATTAG GGTGTATGAG CCTAGCTGGG
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1751 GGGCTTGGGG AGCTTGGAGT GGGGAGAGGG GGTGACTTCT CCGACCAGGC
1801 CTTTCTACCA CCCTACCCTG GGTAAAGGCC TGGAGCAGGA AGCAGCGGCA
1851 AGGACCTCTG GAGCAGCCCA TACCTGCCCT GGCCTGACTC TGCCACTGGC
1901 AGCAGAGTCA ACACAGCAGG TCACTCACA GCAGAGGGCG AAGGCCATCA
1951 TCAGCTCCCT TTATAAGGGA AGGGTCACGC GCTCGGTGTG CCGAGAGTGT
2001 CCTGCTGGT CCTCTGTGCC TGGTGGGGTG GGGGTGCCAG GTGTGTCCAG
2051 AGGAGCCCAG TTGGTAGTGA GGCAGCCATG GGGCTAGAAG CACTGTTGCC
2101 CCTGGCCATG ATAGTGGCCA TCTTCCTGCT CCTGGTGGAC CTGATGCACC
2151 GGCACCAACG CTGGGCTGCA CGTACCCCG CAGTCCCTT GCCACTGCC
2201 GGGCTGGGCA ACCTTGCTGC ATGTGGACTT CCAGAACACA CCATACTGCT
2251 TCGACCAGGT GAGGGAGGAG GTCCTGGAGG GCGGCAGAGG TCCTGAGGAT
2301 GCCCCACCAC CAGCAACAT GGGTGGTGGG TTAAACCACA GGCTGGATCA
2351 GAAGCCAGGC TGAGAAGGGG AAGCAGGTTT GGGGACGTT CCTGGGAAG
2401 GACATTTATA CATGGCATGA AGGACTGGAT TTTCCAAAGG CCAAGGAAGA
2451 GTAGGGCAAG GGCCTGGAGG TGGAGCTGGA CTTGGCAGTG GGCATGCAAG
2501 CCCATTGGGC AACATATGTT ATGGAGTACA AAGTCCCTTC TGCTGACACC
2551 AGAAGGAAAG GCCTTGGGAA TGAAGATGA GTTAGTCCTG AGTGCCGTTT
2601 AAATCACGAA ATCGAGGATG AAGGGGGTGC AGTGACCCGG TTCAAACCTT
2651 TTGCACTGTG GGTCTCTGGG CCTCACTGCT CACCGGCATG GACCATCATC
2701 TGGGAATGGG ATGCTAACTG GGGCCTCTCG GCAATTTTGG TGA CTCTTGC
2751 AAGGTCATAC CTGGGTGACG CATCCAACT GAGTTCCTCC ATCACAAGAG
2801 GTGTGACCCC CACCCCTGCC CCACGATCAG GAGGCTGGGT CTCCTCCTTC
2851 CACCTGCTCA CTCCTGGTAG CCCCAGGGGT CGTCCAAGGT TCAAATAGGA
2901 CTAGGACCTG TAGTCTGGGG TGATCCTGGC TTGACAAGAG GCCCTGACCC
2951 TCCCTCTGCA GTTGGCGGCG CGCTTCGGGG ACGTGTTCAG CCTGCACTG
3001 GCCGTGACGC CATGGTTCGT GCTCAATGGG CTGGCGGCCG TGCGCGAGGC
3051 GATGGTGACC CGCGGCGAGG ACACGGCCGA CCGCCCGCCT GCGCCCATCT
3101 ACCAGGTCCCT GGGCTTCGGG CCGCGTTCCC AAGGCAAGCG GCGGTGGGGG
3151 ACAGAGACCG CGTTTCCGTG GGGCCCGGGT GGACAGTGAC CGTAGCCCAA
3201 CGAGCGCCGA CAGGGCGTGG GGTCTTGAC GTGAAACAGA GATAAAGGCC
3251 AGCGAGTGGG CTGAGGACAG TGGGCCAGGA AACCACCTGC ACGGGGGAGG
3301 TGCGAGTCTG TGGGCTGGGA GGGGGCGGGG CTA CTGCCCCA GACCCGCCAG
3351 AAGCCCGGTG GCGGAGGCTG ATGCGTCGAA GTGGCGGTGG CGGGGACCGC
3401 CCCTATGCTG CGGGCTCAGT GTGGGCGGGA CGGGCGGGAT CTTCTTGAG
3451 TGGAAAGGTG GTCAGGGTGG GCAGAGACGA GGTGGGGCCA AACCCCGCCC
3501 CAGGCAGGGG AGCAATGTGG GTGAGCAAAG AGTGGGCCCT GTGCCAGCT

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3551	GGACCGGGCT	AGGGACTGCG	GGAGACCTTG	TGGAGCGCCA	GGGTTGGAGT
3601	GGGTGGCGGA	GGGTGGGGCC	AAGGCCTTCA	TGGCAACGCC	CACGTGTCCG
3651	TCCCGCCCCC	AGGGGTGATC	CTGTCGCGCT	ATGGGCCCCG	GTGGCGCGAG
3701	CAGAGGCGCT	TCTCCGTGTC	CACCTTGCGC	AACCTGGGCC	TGGGCAAGAA
3751	GTCGCTGGAG	CAGTGGGTGA	CCGAGGAGGC	CGCCTGCCTT	TGTGCCGCTT
3801	CGCCGACCAA	GCCGGTGGGT	GATGGGCAGA	AGGGCACAAA	GCGGGAAGTG
3851	GGAAGGCGGG	GGACGGAGAA	GGCAACCCCT	TACCCGCATC	TCCCCACCCC
3901	CAGGACGCCC	CTTTCGCCCC	AACGGCCTCT	TGGACAAAGC	CGTGAGCAAC
3951	GTGATCGCCT	CCCTCACCTG	CGGGCGCCGC	TTCGAGTACG	ACGACCCTCG
4001	CTTCCTCAGG	CTGCTGGACC	TAGCTCAGGA	GGGACTGAAG	GAGGAGTCGG
4051	GCTTTCTGCG	CGAGGTGCGG	AGCGAGAGAC	CGAGGAGTCT	CTGCAGGGCG
4101	AGCTCCTGAG	AGGTGCCGGG	GCTGGACTGG	GGCCTCCGAA	GGGCAGGATT
4151	TGCATAGATG	GGTTTGGGAA	AGGACATTCC	AGGAGACCCC	ACTGTAAGAA
4201	GGGCCTGGAG	GAGGAGGGGA	CATCTCAGAC	ATGGTCGTGG	GAGAGGTGTG
4251	CCCGGGTCAG	GGGGCACCAG	GAGAGGCCAA	GGAATCTGTA	CCCCCGTCCA
4301	CGTTGGAGAT	TTCGATTTTA	GGTTTCTCCT	CTGGGCAAGG	AGAGAGGGTG
4351	GAGGCTGGCA	CTTGGGGAGG	GACTTGGTGA	GGTCAGTGGT	AAGGACAGGC
4401	AGGCCCTGGG	TCACCTGGA	GATGGCTGGG	GCCTGAGACT	TGTCCAGGTG
4451	AACGCAGAGC	ACAGGAGGGA	TTGAGACCCC	GTTCTGTCTG	GTGTAGGTGC
4501	TGAATGCTGT	CCCGTCCTC	CTGCACATCC	CAGCGCTGGC	TGGCAAGGTC
4551	CTACGCTTCC	AAAAGGCTTT	CCTGACCCAG	CTGGATGAGC	TGCTAACTGA
4601	GCACAGGATG	ACCTGGGACC	CAGCCCAGCC	ACCCCAGAGC	CTGACTGAGG
4651	CCTTCCTGGC	AAAGAAGGAG	AAGGTGAGAG	TGGCTGCCAC	GGTGGGGGGC
4701	AAGGGTGGTG	GGTTGAACGT	CCAGGAGGGA	ATGAGGGGAG	GCTGGGCAAA
4751	AGGTTGGACC	AGTGCATCAC	CCGGCGAGCC	GCATCTGGGC	TGACAGGTGC
4801	AGAATTGGAG	GTCAATTTGGG	GGCTACCCCG	TTCTATCCCC	TGAGTATCCT
4851	CTCGGCCCTG	CTCAGGCCAA	GGGGAGCCCT	GAGAGCAGCT	TCAATGATGA
4901	GAACTTGCCG	ATAGTGGTGG	GTAACCTGTT	CCTTGCCGGG	ATGGTGACCA
4951	CCTCGACCAC	GCTGGCCTGG	GGCCTCCTGC	TCATGATCCT	ACACCTGGAT
5001	GTGCAGCGTG	AGCCCAGCTG	GGGCCCAAGG	CAGGGACTGA	GGGAGGAAGG
5051	GTACAGCTGG	GGGCCCTGG	GCTTAGCTGG	GACACCCGGG	GCTTCCAGCA
5101	CAGGCGTGCG	CAGCGTCCTG	TAAGCCTAAC	TTCTCCAAAC	ACAGGAGGAA
5151	GGAGAGTGTC	CCCTGGGTGC	TGACCCATTG	TGGGGACGCA	TGTCTGTCCA
5201	GTCCGTGTCC	AACAGGAGAT	CGACGACGTG	ATAGGGCAGG	TGCGGCGACC
5251	AGAGATGGGT	GACCAGGCTC	ACATGCCCTA	CACCACTGCC	GTGATTACAG
5301	AGGTGCAGCG	CCTTGGGGAC	ATCATCCCCC	TGAGTGTGAC	CCATATGACA
5351	TCCCGTGACA	TCGAAGTACA	GGGCTTCCGC	ATCCCTAAGG	TAGGCCTGGC
5401	GCCCTCCTCA	CCCCAGCTCA	GCACCAGCAC	CTGGTGATAG	CCCCAGCATG
5451	GCTACTGCCA	GGTGGGCCCA	CTCTAGGAAC	CCTGGCCACC	TAGTCCTCAA
5501	TGCCACCACA	CTGACTGTCC	CCACTTGGGT	GGGGGGTCCA	GAGTATAGGC
5551	AGGGCTGGCC	TGTCCATCCA	GAGCCCCCGT	CTAGTGGGGA	GACAAACCAG
5601	GACCTGCCAG	AATGTTGGAG	GACCCAGCGC	CTGCAGGGAG	AGGGGGCAGT
5651	GTGGGTGCCT	CTGAGAGGTG	TGACTGCGCC	CTGCTGTGGG	GTGCGAGAGG
5701	GTACTGTGGA	CCTTCTCGGG	CGCAGGACTA	GTTGACAGAG	TCCAGCTGTG
5751	TGCCAGGCAG	TGTGTGTCCC	CCGTGTGTTT	GGTGGCAGGG	GTCCCAGCAT
5801	CCTAGAGTCC	AGTCCCCACT	CTCACCCTGC	ATCTCCTGCC	CAGGGAACGA
5851	CATCATCATC	CAACCTGTCA	TCGGTGCTGA	AGGATGAGGC	CGTCTGGGAG
5901	AAGCCCTTCC	GCTTCCACCC	CGAACACTTC	CTGGATGCCC	AGGGCCACTT
5951	TGTGAAGCCG	GAGGCCCTCC	TGCCCTTCTC	AGCAGGTGCC	TGTGGGGAGC
6001	CCGGCTCCCT	GTCCCTTCC	GTGGAGTCTT	GCAGGGGTAT	CACCCAGGAG
6051	CCAGGCTCAC	TGACGCCCTC	CCCTCCTCCA	CAGGCCGCCG	TGATGCCTC
6101	GGGGAGCCCC	TGGCCCGCAT	GGAGCTCTTC	CTCTTCTTCA	CCTCCCTGCT
6151	GCAGCACTTC	AGCTTCTCCG	TGGCCGCCGG	ACAGCCCCGG	CCCAGCCACT
6201	CTCGTGTGCT	CAGCTTTCTG	GTGACCCCAT	CCCCCTACGA	GCTTTGTGCT
6251	GTGCCCGGCT	AGAATGGGGT	ACCTAGTCCC	CAGCCTGCTC	CCTAGCCAGA
6301	GGCTCTAATG	TACAATAAAG	CAATGTGGTA	GTTCCAATT	GGGTCCCCTG
6351	CTCACGCCCT	CGTTGGGATC	ATCCTCCTCA	GGGCAACCCC	ACCCCTGCCT
6401	CATTCTGCT	TACCCACCG	CCTGGCCGCA	TTTGAGACGG	GTACGTTGAG
6451	GCTGAGCAGA	TGTCAGTTAC	CCTTGCCCAT	AATCCCATGT	CCCCACTGA
6501	CCCAACTCTG	ACTGCCCAGA	TTGGTGACAA	GGAATACATT	GTCCTGGCAT
6551	TGCGGGAAGG	GGCCAGAATG	GGCTGACTAG	AGGTGTCACT	CAGCCCTGGA
6601	TGTGGTGGAG	AGGGCAGGAC	TCAGCCTGGA	GGCCCATATT	TCAGGCCTAA
6651	CTCAGCCAC	CCCATATCAG	GGACAGCAGT	CCTGCCAGCA	CCATCACAAC
6701	AGTCACCTCC	CTTCATATAT	GACACCCCAA	AATGGAAGAC	AAATCATGTC
6751	AGGGAGCTAT	ATGCCAGGGC	TACCTCCAG	GGCTCAGTCG	GCAGGTGCCA
6801	GAACATTTCC	TGGGAAGGCC	CCAGGAAAAC	CCAGGACCGA	GCCACCGCCC
6851	TCAGCCTGTC	ACCTTGTGTC	CAAAATTGGT	GGGTTCTTGG	TCTCACTGAC
6901	TTCAAGAAATG	AAGCCGTGGA	CCCTCACGGT	GAGTGTTACA	GTTCTTAAAG
6951	ATGGTGTGTT	CAGAGTTTGT	TCCTTCTGAT	GTTAAGACGT	GTTTCAAGTT
7001	TCTTCTTCT	GGTGGGTGCG	TGGTCTTGCT	GGCTTCAGGA	GTGAAGCTGC
7051	AGACCTTCAC	AGTGAGTGTT	ACGGCTCTTA	AGGCTGCACG	TACGGAGTTG

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7101 TTCATTCTTC CTGGTGGGTT TGTGGTCTCA CTGGCCTCAG GAGTGAAACT
7151 GCAGTCCCTC CAGTGTTACA ACTCATAAAG GCAGTGTGGA CCCAATGAGG
7201 GAGCAGCAGC AGCAAGACTT ACTGCAACA GCAAAAGAAT GATGGCAACC
7251 AGGTTGCCGC TGCTACTTCA GGCAGCCTGC TTTTATTCCC TTATCTGACC
7301 CCCACCCACA TCCTGCTGAT TGGCCCATTT TACAGACAGT GGATTGGTCC
7351 ACTTACAGAG AGCTGATTGG TGCATTTACA ATCCCTGAGC TAGACACAGA
7401 GTACTGATTG GTATATTTAC AAACCTTGAG CTAGACACAG AGTGCTGAAT
7451 GGTGTATTTA CAATCCCTTA GCTAGACATA AAGGTTGTCC CAGTCCCCAC
7501 TAGATTAGCT AGATAGAGTA GACAGAGAGC ACTGATTGGT GCGTTTACAA
7551 ACCTTGAGTT AGACACAGGG TGCTGACTGG TGTGTTTACA AACCTTGAGC
7601 TAGACACAGA GTGCTGATTG GTGTATTTAC AATCTTTTAG CTAGAAATAA
7651 AGGTTCCCCA AGTCCCCACC AGATTAGCTA GATAGAGTGC TAATTGGTGC
7701 ATGCACGAAC CCGGAGCTAG ACACAGAGTG CTGATTGGTG CATATACAAT
7751 CCTCTGGCTA GACATAAAAG TTCTCCAAGT CCCCACCTGA CTCAGGAGCC
7801 CAGCCAGCTT CGCCTAGTGG ATCCTATGCC AGGGCCACAG GCAGAGCTGC
7851 CTGCTAGTCC CACACCGGGC ACCTGTACTC CTCAGCCCTT GGGCAGTGGA
7901 CGGGACCAGG TGCCGTGGAG CAGTGGGAGG CACCCATCCG GGAGGCTCGG
7951 GCCTCGCAGG GAGCCACCG TAGGGAGGCT TGGGCATGGC AGGCTGCAAG
8001 TCCTGAGCCC TGCCCCGCGG GGAGGTGACT GAGGCCTGGC GACAATTCAA
8051 TGCTGGTGAG CGCCGGCAGG CCAGCAGTAC TGGGGGACCC GGTGCCCCCT
8101 CTGCAGCTGC TGGCCAGGT GCTAAGCCCC TCACTGCCTG GGGCCAGAGG
8151 CACCAGCCGG CCGTCCGAG TGCAGGGCCC GCTGAGCCCC TGCCCCACCA
8201 GAACTGGTGC TGGCCCGCA GCAACCCAGG TTCCCGCACA CGCCTCTCCC
8251 TCCATACCTA CCGGCAAGCA GACGGAGCCG GCTCCAGCCT CCACCACTCC
8301 AGAGAGGGGC TCCCACAGTG CAGCGCTGGG CTGAACAAGG TCCTACGCTT
8351 CCAAAGGCTT TTCTGACCC AGCTGGATGA GCTGCTAAT GAGCACAGGA
8401 TGACCTGGGA CCCAGCCCAG CCCCCCGAG ACCTGACTGA GGCCTTTCTT
8451 GGCAGAGATG GAGAAGGTGA GAGTGGCTGC CACGGTGGGG GGCAAGGGTG
8501 GTGGGTTGAG CGTCCCAGGA GGAATGAGGG GAGGCTGGGC AAAAGGTTGG
8551 ACCAGTGCAT CACCCGGCGA GCCGCATCTG GGCTGACAGG TGCAGAATTG
8601 GAGGTCATTT GGGGGCTACC CCGTCTGTCT CCGAGTATGC TCTCGGCCCT
8651 GCTCAGGCCA AGGGGAACCC TGAGAGCAGC TTCAATGATG AGAACCTGCG
8701 CATAGTGGTG GCTGACCTGT TCTCTGCCGG GATGGTGACC ACCTCGACCA
8751 CGCTGGCCTG GGGCTCCTG CTGATGATCC TACATCCGGA TGTGCAGCGT
8801 GAGCCCATCT GGGAAACAGT GCAGGGGCGG AGGGAGGAAG GGTACAGGCG
8851 GGGGCCCATG AACTTTGCTG GGACACCCGG GGCTCCAAGC ACAGGCTTGA
8901 CCAGGATCCT GTAAGCCTGA CCTCCTCCAA CATAGGAGGC AAGAAGGAGT
8951 GTCAGGGCCG GACCCCTGG GTGCTGACCC ATTGTGGGGA CGCATGTCTG
9001 TCCAGGCCGT GTCCAACAGG AGATCGACGA CGTGATAGGG CAGGTGCGGC
9051 GACCAGAGAT GGGTGACCAG GCTCACATGC CCTACACCAC TGCCGTGATT
9101 CATGAGGTGC AGCGCTTTGG GGACATCGTC CCCCTGGGTG TGACCCATAT
9151 GACATCCCGT GACATTCGAA GTACAGGGCT TCCGCATCCC TAAGGTAGGC
9201 CTGGCGCCNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
9251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
9301 NNNNNNNCCT GCCCAGGGAA CGACACTCAT CACCAACCTG TCATCGGTGC
9351 TGAAGGATGA GGCCGTCTGG GAGAAGCCCT TCCGCTTCCA CCCCAGACAC
9401 TTCTTGGATG CCCAGGGCCA CTTTGTGAAG CCGGAGGCCT TCCTGCCTTT
9451 CTCAGCAGGT GCCTGTGGGG AGCCCGGCTC CCTGTCCCTT TCCGTGGAGT
9501 CTTGCAAGGG TATCACCAG GAGCCAGGCT CACTGACGCC CCTCCCTCC
9551 CCACAGGCCG CCGTGCATGC CTCGGGGAGC CCCTGGCCCG CATGGAGCTC
9601 TTCTCTTTCT TCACCTCCCT GCTGCAGCAC TTCAGCTTCT CGGTGCCCCA
9651 TGGACAGCCC CGGCCAGCC ACCATGGTGT CTTTGCTTTC CTGGTGAGCC
9701 CATCCCCCTA TGAGCTTTGT GCTGTGCCCC GCTAGAATGG GGTACCTAGT
9751 CCCCAGCCTG CTCCCTAGCC AGAGGCTCTA ATGTACAATA AAGCAATGTG
9801 GTAGTTCCAA CTCGGGTCCC CTGCTCACGC CCTCGTTGGG ATCATCTCTC
9851 TCAGGGCAAC CCCACCCCTG CCTATTCTT GCTTACCCCA CCGCCTGGCC
9901 GCATTTGAGA CAGGGGTACG TTGAGGCTGA GCAGATGTCA GTTACCCTTG
9951 CCCATAATCC CATGTCCCCC ACTGACCCAA CTCTGACTGC CCAGATTGGT
10001 GACAAGGACT ACATTGTCTT GGCATGTGGG GAAGGGGCCA GAATGGGCTG
10051 ACTAGAGGTG TCACTCAGCC CTGGATGTGG TGGAGAGGGC AGGACTCAGC
10101 CTGGAGGCCC ATATTTCAGG CCTAACTCAG CCCACCCAC ATCAGGGACA
10151 GCAGTCTGCG CAGCACCATC ACAACAGTCA CCTCCCTTCA TATATGACAC
10201 CCAAAAACGG AAGACAAATC ATGGCGTCAG GGAGCTATAT GCCAGGGCTA
10251 CCTACCTCCC AGGGCTCAGT CGGCAGGT

(SEQ ID NO: 3)

FEATURES:

Start.....2078
Exon: 2078-2258
Intron: 2259-2961
Exon: 2962-3133

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Intron: 3134-3903
Exon: 3904-4064
Intron: 4065-4496
Exon: 4497-4673
Intron: 4674-4865
Exon: 4866-5007
Intron: 5008-5201
Exon: 5202-5389
Intron: 5390-5843
Exon: 5844-5985
Intron: 5986-9556
Exon: 9557-9732
Stop 9733

SNPs:

DNA Position	Major	Minor	Domain	Protein Position	Major	Minor
3101	C	T A	Exon	107	T	T T
3439	A	G	Intron			
4908	C	T	Exon	245	P	L
5627	G	A	Intron			
6733	T	C	Intron			
7788	-	C T	Intron			
7867	G	A	Intron			
7948	C	T	Intron			

Context:

DNA
Position

3101 GTGTGACCCCCACCCCTGCCCCACGATCAGGAGGCTGGGTCTCCTCCTTCCACCTGCTCA
CTCCTGGTAGCCCCGGGGGTTCGTCCAAGGTTCAAATAGGACTAGGACCTGTAGTCTGGGG
TGACTCTGGCTTGACAAGAGGCCCTGACCCTCCCTCTGCAGTTGCGGCGCCGCTTCGGGG
ACGTGTTTACAGCTGCAGCTGGCCTGGACGCCGGTGGTCTGCTCAATGGGCTGGCGGCCG
TGCGCGAGGCGATGGTGACCCGCGGCGAGGACACGCCCGACCGCCCGCTGCGCCCATCT
[C, T, A]
CCAGGTCTGGGCTTCGGGCCGCGTTCCCAAGGCAAGCGGCGGTGGGGACAGAGACCGC
GTTTCCGTGGGCCCCGGGTGGACAGTGACCGTAGCCCAAGCAGCGCCGACAGGGCGTGGG
GTCTTGACGTGAAACAGAGATAAAGGCCAGCGAGTGGGCTGAGGACAGTGGGCCAGGAA
ACCACCTGCACGGGGGAGGTGCGAGTCTGTGGGCTGGGAGGGGGCGGGGCTACTGCCAG
ACCCGCCAGAAGCCCGGTGGGCGAGGCTGATGCGTCGAAGTGGCGGTGGCGGGACCGCG
(nt 2801-3401 of SEQ ID NO: 3)

3439 CGGCGGTGGGGGACAGAGACCGCGTTTCCGTGGGCCCCGGGTGGACAGTGACCGTAGCCC
AAGCAGCGCCGACAGGGCGTGGGGTCTTGACGTGAAACAGAGATAAAGGCCAGCGAGTG
GGCTGAGGACAGTGGGCCAGGAAACACCTGCACGGGGGAGGTGCGAGTCTGTGGGCTGG
GAGGGGGCGGGGCTACTGCCAGACCCGCCAGAAGCCCGGTGGGCGAGGCTGATGCGTCG
AAGTGCGGTTGGCGGGACCGCGCTATGCTGCGGGCTCAGTGTGGGCGGGACGGCGGG
[A, G]
TCTTCCCTTGTAGTGAAAGGTGGTCAGGTTGGGCGAGAGACGAGTGGGGCCAAACCCGCC
CCAGGCAGGGGAGCAATGTGGGTGAGCAAAGAGTGGGCCCTGTGCCAGCTGGACCGGGC
TAGGGACTGCGGGAGACCTTGTGGAGCGCCAGGGTTGGAGTGGGTGGCGGAGGGTGGGGC
CAAGGCCTTATGGCAACGCCACGTGTCCGTCCCGCCCCAGGGGTGATCCTGTGCGGC
TATGGGCCCGCGTGGCGCGAGCAGAGGCGCTTCTCCGTGTCCACCTGCGCAACTTGGGC
(nt 3139-3739 of SEQ ID NO: 3)

4908 ATGACCTGGGACCCAGCCAGCCACCCGAGACCTGACTGAGGCCTTCCTGGCAAAGAAG
GAGAAGGTGAGAGTGGCTGCCACGTTGGGGGGCAAGGGTGGTGGGTTGAACGTCCCAGGA
GGAATGAGGGGAGGCTGGGCAAAAGGTTGGACCAAGTGCATCACCCGGCGAGCCGCATCTG
GGCTGACAGGTGCAGAATTGAGGTCATTTGGGGGCTACCCCGTTCTATCCCTGAGTAT
CCTCTCGGCCCTGCTCAGGCCAAGGGGAGCCCTGAGAGCAGCTTCAATGATGAGAACCTG
[C, T]
GCATAGTGGTGGGTAACTGTTCCTTGCCGGGATGGTGACCACCTCGACCACGCTGGCCT
GGGGCTCCTGCTCATGATCCTACACCTGGATGTGCAGCGTGAGCCAGCTGGGGCCCAA
GGCAGGACTGAGGGAGGAAGGTTACAGCTGGGGGGCCCTGGGCTTAGCTGGGACACCCG
GGGCTTCCAGCACAGCGTGGCCAGGCTCCTGTAAGCCTAACTTCCTCAACACAGGAGG
AAGGAGAGTGTCCCTGGGTGCTGACCCATTGTGGGGACGCATGTCTGTCCAGTCCGTGT
(nt 4608-5208 of SEQ ID NO: 3)

Replacement Sheet
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- 5627 CCCCTGAGTGTGACCCATATGACATCCCGTGACATCGAAGTACAGGGCTTCCGCATCCCT
AAGGTAGGCCTGGCGCCTCCTCACCCTCAGCTCAGCACCAGCACCTGGTGATAGCCCCAG
CATGGTACTGCCAGGTGGGCCCCACTCTAGGAACCTGGCCACCTAGTCTCAATGCCAC
CACACTGACTGTCCCCACTTGGGTGGGGGTCCAGAGTATAGGCAGGGCTGGCCTGTCCA
TCCAGAGCCCCCGTCTAGTGGGGAGACAAACCAGGACCTGCCAGAAATGTTGGAGACCCA
[G,A]
CGCCTGCAGGGAGAGGGGGCAGTGTGGGTGCCTCTGAGAGGTGTGACTGCGCCCTGCTGT
GGGGTTCGAGAGGGTACTGTGGAGCTTCTCGGGCGCAGGACTAGTTGACAGAGTCCAGCT
GTGTGCCAGGCAGTGTGTGTCCCCGTGTGTTTGGTGGCAGGGGTCCCAGCATCTAGAG
TCCAGTCCCCACTCTACCCCTGCATCTCCTGCCAGGGAACGACACTCATACCAACCTG
TCATCGGTGCTGAAGGATGAGGCCGTCTGGGAGAAGCCCTTCCGCTTCCACCCCGAACAC
(nt 5237-5927 of SEQ ID NO: 3)
- 6733 TGAGACGGGTACGTTGAGGCTGAGCAGATGTCACTTACCCTTGCCCATATCCCATGTCC
CCCCTGACCCCAACTCTGACTGCCCAGATTGGTGACAAGGACTACATTGTCTGGCATGT
GGGGAAGGGGCCAGAAATGGGCTGACTAGAGGTGTCACTCAGCCCTGGATGTGGTGGAGAG
GGCAGGACTCAGCCTGGAGGCCCATATTTTCAGGCCTAACTCAGCCACCCACATCAGGG
ACAGCAGTCTGCCAGCACCATCACAAACAGTCACCTCCCTTCATATATGACACCCCAAAA
[T,C]
GGAAGACAAATCATGTGAGGGAGCTATATGCCAGGGCTACCTCCCAGGGCTCAGTCGGCA
GGTGCCAGAACATTCCCTGGGAAGGCCCCAGGAAACCCAGGACCGAGCCACCGCCCTCA
GCCTGTCACTTGTGTCCAAATTTGGTGGGTTCTTGGTCTCACTGACTTCAAGATGAAG
CCGTGGACCCCTCAGCGTGAGTGTACAGTTCTTAAAGATGGTGTGTTCAGAGTTTGTTC
TTCTGATGTTAAGACGTGTTTCAAGTTTCTTCTTCTGGTGGGTGCGTGGTCTTGTGGC
(nt 6433-7033 of SEQ ID NO: 3)
- 7788 TCCAGTCCCCACTAGATTAGCTAGATAGAGTAGACAGAGGACTGATTGGTGC GTTTA
CAAACCTTGAGTTAGACACAGGGTGTGACTGGTGTGTTTACAAACCTTGAGCTAGACAC
AGAGTGTGATTGGTGTATTTACAATCTTTTAGCTAGAAATAAAGGTTCCCCAAGTCCCC
ACCAGATTAGCTAGATAGAGTGCTAATTGGTGCATGCACGAACCCGGAGCTAGACACAGA
GTGCTGATTGGTGCATATACAATCCTCTGGCTAGACATAAAAGTTCTCCAAGTCCCCACC
[-,C,T]
GACTCAGGAGCCCAGCCAGCTTCGCCTAGTGATCCTATGCCAGGGCCACAGGCAGAGCT
GCCTGTGACTCCACACCGGGCACCCTGTACTCCTCAGCCCTTGGGCAGTGGACGGGACCA
GGTGCCGTGGAGCAGTGGGAGGCACCCATCCGGGAGGCTCGGGCCTCGCAGGGAGCCAC
CGTAGGGAGGCTTGGGCATGGCAGGCTGCAAGTCTTGAGCCCTGCCCCGCGGGGAGGTGA
CTGAGGCCTGGCGACAATTCAAGTGTGGTGAGCGCCGCGCAGGCCAGCAGTACTGGGGGAC
(nt 7488-8088 of SEQ ID NO: 3)
- 7867 AGGGTGTGACTGGTGTGTTTACAAACCTTGAGCTAGACACAGAGTGTGATTGGTGTAT
TTACAATCTTTTAGCTAGAAATAAAGGTTCCCCAAGTCCCCACCAGATTAGCTAGATAGA
GTGCTAATTGGTGCATGCACGAACCCGGAGCTAGACACAGAGTGTGATTGGTGCATATA
CAATCCTCTGGCTAGACATAAAAGTTCTCCAAGTCCCCACCTGACTCAGGAGCCAGCCA
GCTTCCGCTAGTGGATCCTATGCCAGGGCCACAGGCAGAGCTGCCTGCTAGTCCACACC
[G,A]
GGCACCTGTACTCCTCAGCCCTTGGGCAGTGGACGGGACCAGGTGCGGTGGAGCAGTGGG
AGGCACCCATCCGGGAGGCTCGGGCCTCGCAGGGAGCCACCGTAGGGAGGCTTGGGCAT
GGCAGGCTGCAAGTCTGAGCCCTGCCCCGCGGGGAGGTGACTGAGGCCTGGCGACAATT
CAAGTGTGGTGAAGCGCGGAGGCCAGCAGTACTGGGGGACCCGGTGGCCCTCTGCAGC
TGCTGGCCAGGTGCTAAGCCCTCACTGCCTGGGGCCAGAGGCACCGCCGCGGCTCC
(nt 7567-8167 of SEQ ID NO: 3)
- 7948 TAAAGGTTCCCCAAGTCCCCACCAGATTAGCTAGATAGAGTGTGTAATTGGTGCATGCACG
AACCCGGAGCTAGACACAGAGTGCTGATTGGTGCATATACAATCCTCTGGCTAGACATAA
AAGTTCTCCAAGTCCCCACCTGACTCAGGAGCCAGCCAGCTTCGCTAGTGGATCCTAT
GCCAGGGCCACAGGCAGAGCTGCCTGCTAGTCCACACCGGGCACCTGTACTCCTCAGCC
CTTGGGCAGTGGACGGGACCAGGTGCCGTGGAGCAGTGGGAGGCACCCATCCGGGAGGCT
[C,T]
GGGCCTCGCAGGGAGCCACCGTAGGGAGGCTTGGGCATGGCAGGCTGCAAGTCTTGAGC
CTGCCCCGCGGGGAGGTGACTGAGCCTGGCGACAATTCAAGTGTGGTGAAGCGCCGCA
GGCCAGCAGTACTGGGGGACCCGGTGGCCCTCTGCAGCTGCTGGCCAGGTGCTAAGCC
CCTCACTGCCTGGGGCCAGAGGCACAGCCGCGCCGCTCCGAGTGCAGGGCCCGCTGAGCC
CCTGCCACCCAGAACTGGTGTGCTGGCCGCGAGCAACCCAGGTTCCCGCACACGCTCTC
(nt 7648-8248 of SEQ ID NO: 3)

Chromosome mapping:
Chromosome #22